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ANALYSING THE EFFECT OF ENVIRONMENTAL VARIABILITY ON ANNUAL FISH GROWTH RATES IN QUEENSLAND'S DRYLAND RIVERS

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HAWWA RAUFATH NIZAR

SUPERVISORS: DR. REBECCA CAMP (UQ), DR. KATE HODGES (DES) AND DR. JONATHON MARSHALL (DES)
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Abstract

This study examines the impact of environmental and hydrological variability on the growth rates of three fish species—Golden Perch, Bony Bream, and Common Carp—across 11 sites within the Northern Murray-Darling Basin, using otolith-derived annual growth rates as a proxy. Focusing on physicochemical properties such as temperature and stream flow, I modeled growth responses to these variables, revealing significant interspecies differences. Results indicate that Bony Bream, with its suitability to the semi-arid dryland riverine habitats, displayed higher growth rates compared to the invasive Common Carp and migratory Golden Perch. The study underscores the necessity of species-specific management strategies and highlights the complexity of interactions within these ecosystems, suggesting that integrated approaches considering multiple environmental factors are essential for effective management and conservation. The research provides a foundation for future investigations into the ecological dynamics of fish growth in response to climate variability and hydrological changes.

Introduction

The complex interplay between spatial and temporal variability in physicochemical properties of the environment, and their influence on growth of various marine species has been the subject of extensive research (Jobling 2002; Canosa and Bertucci 2023). Concurrently, the growing evidence of shifting thermal and precipitation regimes, along with the intensification of extreme climate and weather events, (Saintilan et al. 2013; Westra et al. 2014; Vousdoukas et al. 2018; Zhou et al. 2019; IPCC 2022), suggests increased potential for disruptions in ecosystem functions that are strongly linked to growth, such as spawning (Steel et al. 2019), nutrient cycling (D’Odorico et al. 2003) and overall ecosystem productivity (Woodward et al. 2016; Gampe et al. 2021). In lotic habitats such as dryland river systems, these influences are compounded by inherent environmental variability in key abiotic parameters such as turbidity, substrate composition, temperature and most notably, hydrology (Maestre et al. 2012; Lapointe et al. 2014). The distinctive hydrological characteristics of dryland rivers create cyclic conditions of “booms” in productivity due, in part, to episodic floods, followed by “bust” periods after the waters recede, leaving behind perennial and semi-perennial waterholes. During drought periods, these waterholes serve as refuges for many aquatic species (Sheldon et al. 2010; Arthington and Balcombe 2011). Most of these dryland riverine ecosystems experience long periods of low to no-flow (Douglas et al. 2005; Kennard et al. 2010; Morón and Amos 2018), and remain as disconnected refuges for most of the year, with some persisting over several years with no surface flow (Bunn et al. 2006a, 2006b). Though the term ‘refuge’ here is used to denote “places (or times) where the negative effects of disturbance are lower than in the surrounding area (or time)” (Lancaster and Belyea 1997; Sheldon et al. 2010), the isolated, relatively small and densely populated nature of such refuges can introduce novel stressors and intensify existing ones. For instance, research conducted on similar remote habitats suggest that food web interactions, including predator prey interactions are heightened during such cases (Jackson et al. 2001; Magoulick and Kobza 2003; Gido et al. 2015), particularly where species are present in high densities. These impacts have also been

documented across a host of other biotic processes and interactions, such as exposure to disease and parasites, competition, and migration (Magoulick and Kobza 2003; Arthington and Balcombe 2011). Sudden and often severe changes in these processes have been associated with fish mortality in such dryland refuges (Wager and Unmack 2000; Magoulick and Kobza 2003; Balcombe et al. 2005; Turschwell et al. 2019). Furthermore, the size and nature of such water bodies can also play a critical role in exacerbating abiotic stressors; the biogeographically insular nature of the refuges themselves can alter much of the physicochemical and biological properties of the habitat (Magoulick and Kobza 2003). For example, not only are smaller water bodies known exhibit a higher degree of temporal variation in oxygen and temperature (Jackson et al. 2001), the increased evaporation and low-flow associated with such water bodies can cause increased sedimentation, salinity and turbidity (Wager and Unmack 2000; Pettit et al. 2012), all of which can potentially contribute to low growth and survival.

Despite their highly variable hydrology and the consequential, often harsh, conditions, these are critically important and highly biodiverse ecosystems that have shaped (Macklin and Lewin 2015; Moggridge and Thompson 2021) and continue to shape not just land-use, sustenance, and livelihoods, but also the cultural values and heritage of the surrounding communities (Anderson et al. 2019). Furthermore, the ecosystem processes of these habitats are greatly influenced by this variability; from dispersal regimes (Petty and Grossman 2004), to spawning (Franssen et al. 2007), to primary production (Balcombe et al. 2015). Hence, investigating the survival, growth, and reproductive success of different species within these habitats is paramount to understanding their response to the frequency and intensity of such disturbance events.

The widespread occurrence of these habitats also underscores the need to focus research efforts on them. Approximate 83% of all 3.5 million kilometres of Australian low land rivers (when mapped at a scale of 1:250,000) have been classified as dryland rivers; that is to say, they are primarily found in arid to semi-arid regions (Thoms and Sheldon 2000; Sheldon et al. 2010). The Murray-Darling Basin alone, where this research project is centred, supports agricultural production valued at AUD 30 billion per year (Murray–Darling Basin Authority

2023). Given the high economic and ecological significance of these habitats, research on non-perennial and semi-perennial rivers in Australia has spanned a vast array of topics, demonstrating clear trends in evolving research focus over the past several decades (Shanafield et al. 2024). Much of the work focusses on the role of waterholes as refuges, and how various aspects of fluvial geomorphology contribute to their suitability as such. This includes research into factors that contribute to their persistence, such as groundwater discharge (Davis et al. 2021; Bourke et al. 2023), bank return flow (Rhodes et al. 2017; Zhou and Cartwright 2021) and drainage and evaporation rates (Hamilton et al. 2005; Brunner et al. 2009). Many papers also report on the response of various species to the hydrological and environmental variability, including the effect of these extreme conditions on various biological processes, such as migration (Marshall et al. 2016), dispersal regimes (Faulks et al. 2010; Chester et al. 2015; Razeng et al. 2017), reproduction and fecundity (Mooij et al. 2002). Works focussing on factors affecting growth of species in dryland river systems includes research on the interactions between growth and extreme high temperatures (Wallace et al. 2015), as well as comparative inter-species and inter-site analyses (Mallen-Cooper and Stuart 2003; Koehn 2004). Reviews focussed on the Murray-Darling Basin note that much of the data requires updating and highlight the need for further research into factors that affect fish growth (Koehn et al. 2019, 2020). Amid this broad spectrum of research, this project aims to add to the current repository of knowledge by deepening our understanding of the impact of various environmental and hydrological factors on, growth rate of three species across 11 sites in rivers in the Northern Murray-Darling Basin; Golden perch (*Macquaria ambigua*), Bony bream (*Nematalosa erebi*) and Common carp (*Cyprinus carpio*). This research not only models the impact of multiple environmental predictor variables on the growth rates of fish species, but also includes both native and non-native species, thus offering a robust dataset for comparative analysis, providing valuable insights into how different species respond to similar environmental pressures in dryland river systems.

Given the complex nature of interactions between environmental factors and species growth that are expected, reliable and quantifiable methods of measuring growth is

required. Especially since monitoring growth and movement in fish populations can be particularly challenging when the species in question exhibit migratory behaviour. Sclerochronological studies, which analyse incremental marks on calcified structures, are one method utilised to address this issue. In particular, otolith (ear bone) growth rings are widely researched and recognised as effective proxies for tracking fish growth, as well as the impact of pertinent environmental parameters such as temperature (Gillanders et al. 2012; Martino et al. 2019; Morrongiello et al. 2019; Dunlop et al. 2023). As such, otolith biochronology is used in this project as a proxy measure for examining the impact of various hydrological and environmental factors and their spatiotemporal variability, on incremental growth rates in the aforementioned three species. Specifically, incremental growth rings on otoliths were visualised and measured using high-precision tools, and the results were then converted into annual growth rates, to be used in the modelling process as the response variable.

Methods and Approach

2.1 Study Area and Data Sources

This analysis encompassed data from a total of 11 sites (see Table 1, Figure 1), all of which were located across south and west Queensland, except for one site in New South Wales (Site ID: 5). Each site features specific hydrological control structures, which are critical in managing water flow and sediment transportation and can thus potentially affecting habitat conditions and fish growth rates. Although this report does not look at the effect of different modes of control on discharge volumes and patterns, there is a notable variety in controls across the sites, from crump weirs, which are a more specialized and precise means of control designed to manage flow rates accurately (Caroline and R Afshar 2014; Bachir and Lyes 2022), to more general and traditional controls such as sand, timber and mud.

The range of ecological and environmental datasets utilized for this project was derived from three main sources:

2.1.1 Microsoft Power BI Solution Developed by La Trobe University

All of data on the response variable, otolith-derived annual growth rates from age 1 to age 2 for the three fish species, was accessed and extracted via a cloud-based data dashboard developed using Microsoft Power BI. This dashboard was developed by La Trobe University, with input from the Department of Environment and Science (DES), Queensland. The otolith data was collected twice across the 11 sites, once in 2020 and once in 2021, following the drought of 2018, which resulted in a significant decrease in rainfall across the region (DAFF 2018). This analysis primarily utilized two datasets derived from an initial dataset of 1,658 data points. These datasets were tailored to meet specific study conditions, focusing on individuals no younger than 2 years old in 2021. The first dataset, containing 819 data points, excluded all instances of zero growth rates. The second dataset retained these zero growth rates, resulting in 1,367 data points. Additionally, the La Trobe dataset also included some of the predictor variables utilised for this analysis, most notably streamflow and stream level

data for 2020-2021, which was sourced from stream gauges installed within the study area. A total of ten gauges were utilised to extract data on 11 sites (see Figure 1).

SITE ID	GAUGE ID	RIVER	CONTROL	LATITUDE	LONGITUDE
1	422201F	Balonne river at St. George	Crump Weir	-28.0614	148.5636
2	423204A	Warrego river at Augathella	Sand	-25.7928	146.5857
3	422205A	Balonne-minor river at Hastings	Sheet Piling Weir	-28.4312	148.2742
4	422206A	Narran river at Dirranbandi-Hebel Road	Mud	-28.8402	148.0525
5	422015	Culgoa river at Brenda	Historic weir (wooden + earthfill)	-29.0296	147.3135
6	422207A	Ballandool river at Hebel Bollon Road	Mud	-28.9377	147.7524
7	422207A	Ballandool river at Hebel Bollon Road	Mud	-28.9377	147.7524
8	422211A	Briarie Creek at Woolerbilla-Hebel Road	Sand And Mud	-28.9081	147.6889
9	422209A	Bokhara river at Hebel	Rock and concrete storage Weir	-28.9694	147.7973
10	417205A	Moonie river at Flinton	Mud and Timber	-27.8944	149.5254
11	422202B	Dogwood Creek at Gilweir	Storage Ogee Weir	-26.7089	150.1792

Table 1: List of all sites utilised for the study, alongside information on the stream gauges, the locations of the sites, and the form of hydrological control utilised at them

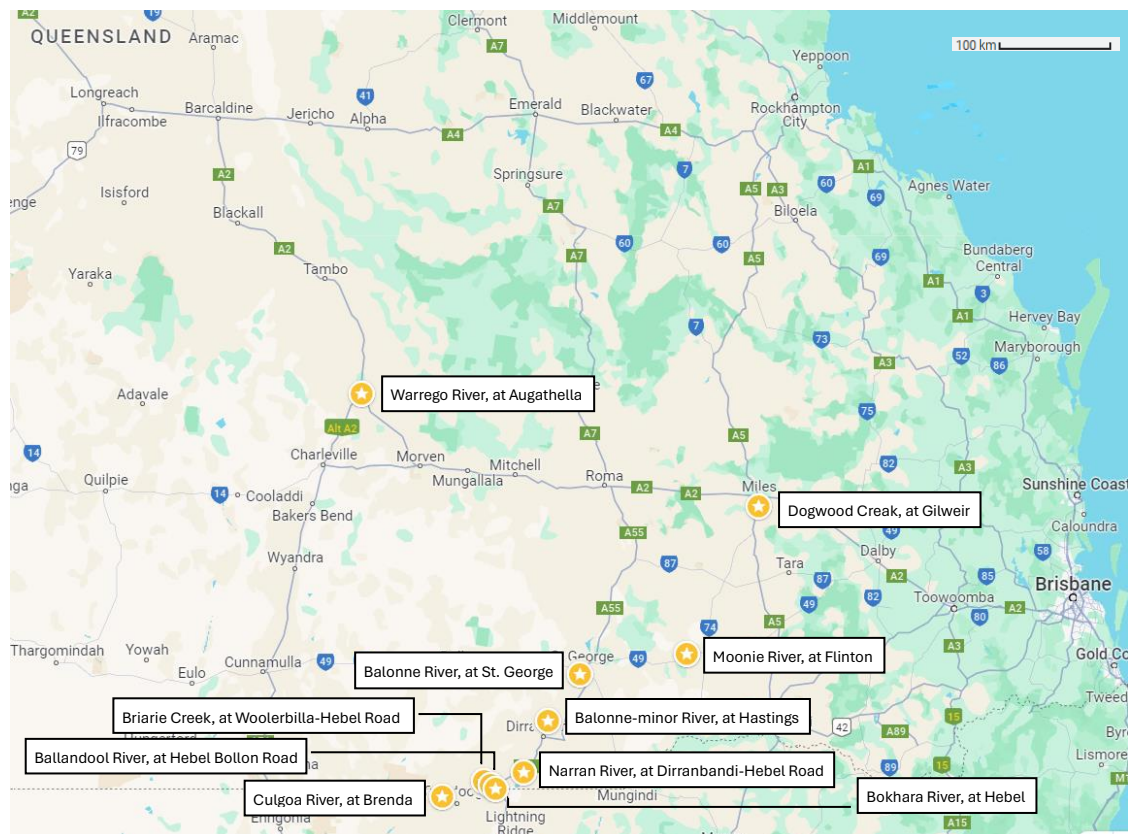


Figure 1: Map showing the location of 10 stream gauges, used to extract data for the 11 study sites where otolith data was collected. Google (2024) Queensland. Available at: <http://maps.google.co.au> (Accessed: 5 May 2024).

2.1.2 SILO Database

Data on annual rainfall and evaporation levels was extracted from the SILO database, which is maintained by the Queensland Government and carries information on a host of environmental variables for the region, from 1889 to present day (Queensland Government 2024a). As this analysis specifically examines the annual growth rate from year 1 to 2, data was downloaded for the period 2000-2021, covering this life history stage for all the fish of varying age.

2.1.3 Water Monitoring Information Platform (WMIP)

The WMIP platform, which is also maintained by the Queensland Government and integrates data from various gauges across Queensland (Queensland Government 2024b), was mainly used to access minimum, maximum, and mean water levels across the study sites, for both the duration of the study and the years immediately preceding it. This data was then analysed to identify temporal patterns and trends in water levels, and to calculate the number of zero-flow days and the longest no-flow spells each year for the period 2000-2021.

2.2 Data Preparation and Basic Exploratory Data Analysis

Prior to analysis, the data from all three sources was cleaned, prepared and consolidated. For cases with multiple sets of similarly formatted repetitive data, such as the SILO and WMIP gauge datasets, the data was read-in using specifically constructed loops, with the intention of reusing the code snippet for similar projects, given the format of raw data files remains consistent. As discussed above, some data sets such as the daily stream level data and the cease-to-flow level data was used to construct new predictor variables such as number of no-flow days per year and longest no flow periods per year.

After completing basic data cleaning and structuring tasks, 1,367 data points were retained, distributed by species as seen in Figure 2. However, it was also noted that a large part of this

data included zero counts for annual growth rate ($n = 547$), which was distributed by species and site, as seen in Figure 3.

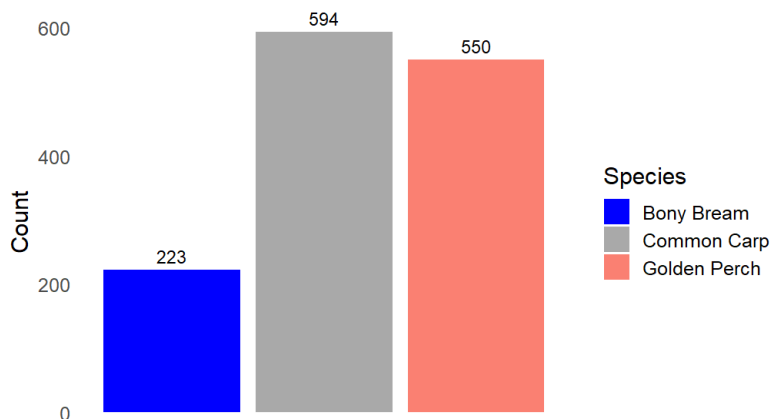


Figure 2: Count of three fish species in study sample: Bony Bream (223), Common Carp (594), and Golden Perch (550).

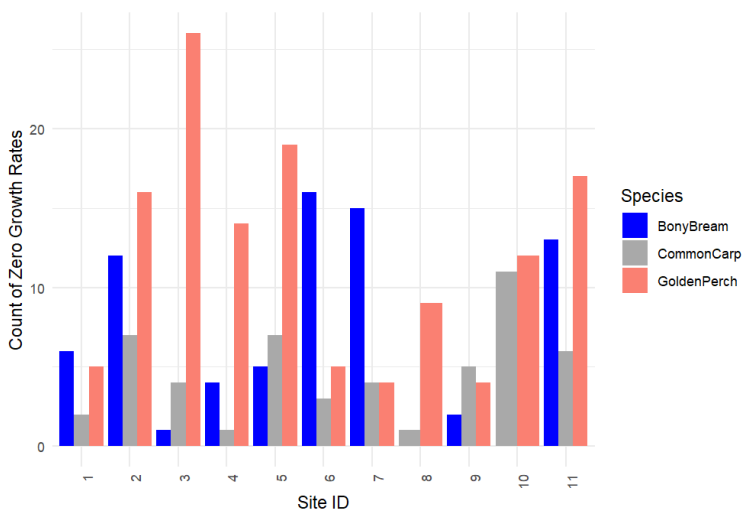


Figure 3: Count of zero growth rate across different site IDs for three fish species; each bar represents the total counts of observed zero growth rate for each species at each site. Sites 3, 5, and 11 exhibit relatively higher counts of zero growth rate for Golden Perch, indicating potential site-specific factors affecting their growth.

Following this, I visualised the data using scatterplots, to examine the spread of data, and identify and visually obvious relationships or patterns. While the temperature variables did not show strong linear correlation with annual growth (see Figure 4), the fitted smoothing lines do indicate the presence on nonlinear relationships across the board. These patterns varied not only by species, but also by life history stage, with notable peaks at 21°C for bony bream at age 2 and spawning, which is aligned with research findings on prime spawning

temperature for bony bream (Rayner et al. 2015). The clusters evident in the plots could also further indicate that specific temperature ranges might influence growth rates more significantly.

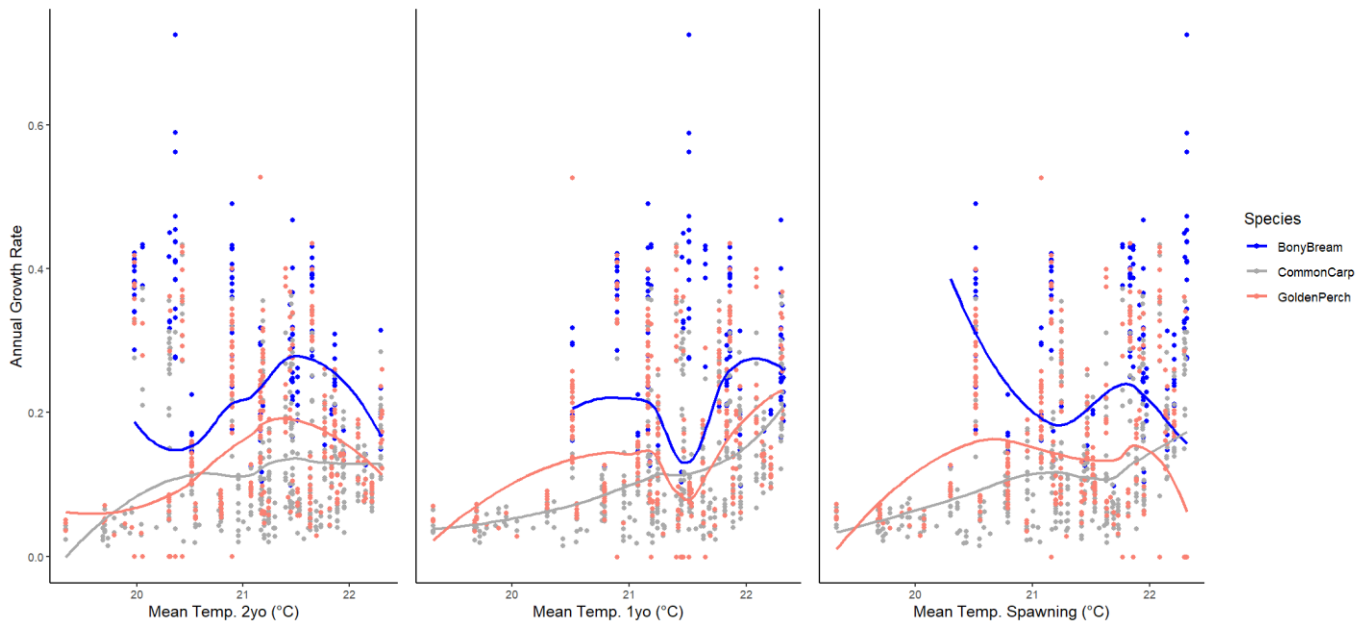


Figure 4: Relationship between annual growth rate of three fish species (Bony Bream, Common Carp, and Golden Perch) and mean temperature at different life stages: 2 years old (2yo), 1 year old (1yo), and during spawning

The scatterplots also indicated potential nonlinear relationships between the longest zero-flow periods and annual growth rate (see Figure 5). These patterns also varied by species and life history stage, as with temperature variables. Annual Growth rate for Bony Bream exhibits distinct peaks and dips, particularly during age 2 years. Common Carp and Golden Perch exhibit more stable growth rates across the range of zero-flow durations, though some nonlinear patterns can be observed.

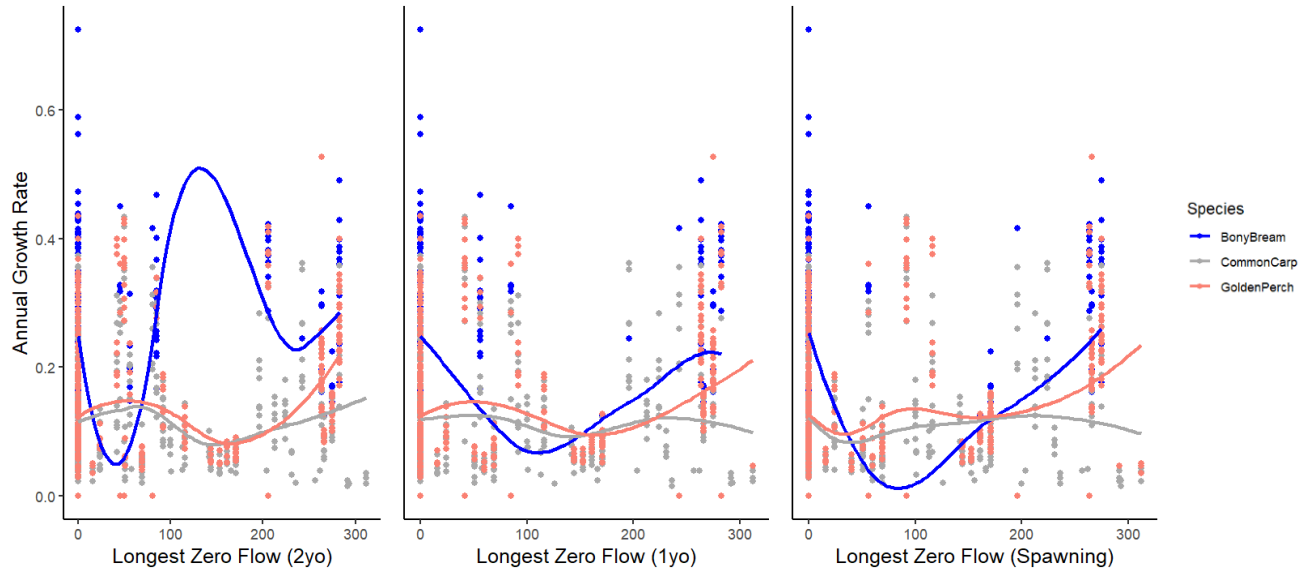


Figure 5: Relationship between the annual growth rate of three fish species (Bony Bream, Common Carp, and Golden Perch) and the longest zero-flow periods at different life stages: 2 years old (2yo), 1 year old (1yo), and during spawning.

The boxplots generated indicate that Bony Bream (0.21) has a higher median annual growth rate compared to Common Carp (0.09) and Golden Perch (0.11) (see Figure 6). However, there did not appear to be a visually apparent significant difference between the interspecific growth rates, as the overlap in the interquartile ranges and the presence of outliers suggest variability within each species.

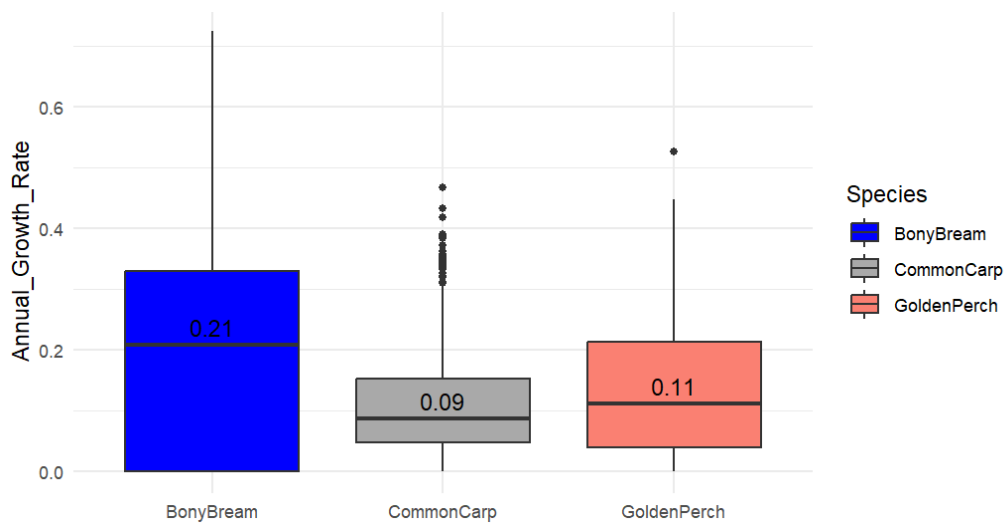


Figure 6: Distribution of annual growth rates across the three fish species. Bony Bream shows a higher median annual growth rate (0.21) compared to Common Carp (0.09) and Golden Perch (0.11)

I also generated a correlation matrix for the data to determine which variables had high levels of correlation. The exercise revealed a high degree of correlation amongst the predictor variables (see Figure 7). The streamflow variables which were derived from daily flow data (Longest Zero Flow, Zero Flow Days) exhibit high positive correlation (0.81-0.98), while evaporation (mm) and average daily rain (mm) are seen to have strong negative correlation (-0.89). Thus, several strategies were employed to address the risk of multicollinearity and improve the integrity and robustness of the models. Aside from the Principal Component Analysis (PCA) which was used to reduce dimensionality and address multicollinearity in some of the models, highly correlated predictor variables were also eliminated or used alternatingly in other iterations of the models, based on model performance and the correlation matrix below.

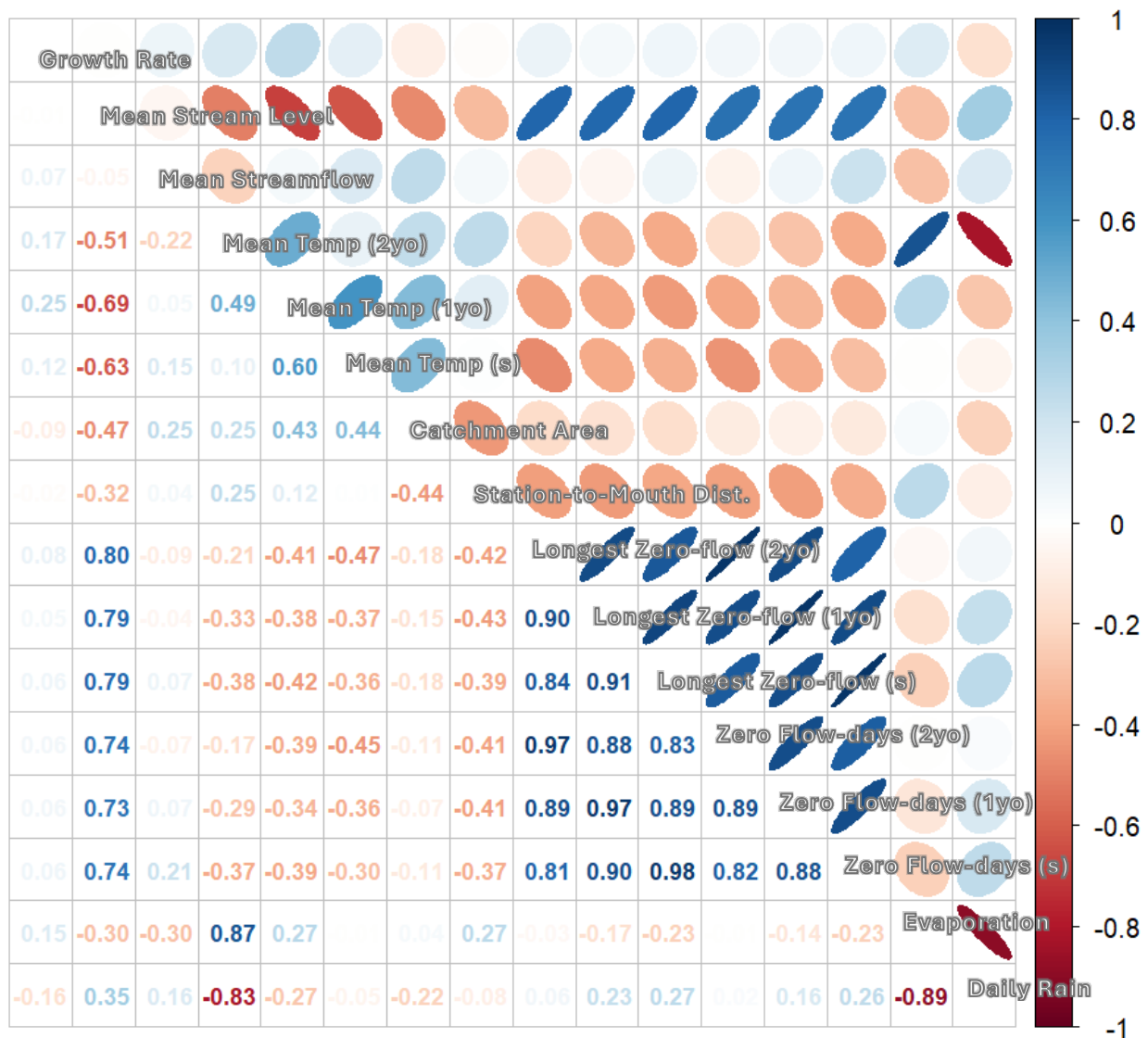


Figure 7: Correlation matrix displaying pairwise correlation coefficients between the full set of response and predictor variables. Blue areas represent high positive correlation, while red indicates high negative correlation. The streamflow variables which were derived from daily flow data (Longest Zero Flow, Zero Flow Days) exhibit high positive correlation (0.81-0.98), while evaporation (mm) and average daily rain (mm) are seen to have strong negative correlation (-0.89).

2.3 Modeling

The modeling process, as discussed above, was iterative, starting with simple, untransformed variables and linear models, and gradually progressing to more complex model structures, such as Generalized Linear Models (GLMs), and Bayesian GLMs that tested transformed variables, non-linear relationships, predictor variables derived from Principal Component Analysis (PCA), polynomial terms, and interaction terms. The aim of this process was not only to progressively determine the effect of various hydrological and environmental factors on annual growth rate, in the three species of interest, but also to gradually improve model fit and develop a model that explains the maximum possible variability in the response variable. The full suite of models fitted are available via the R script which is linked at the end of this report.

2.3.1 Linear Models

The initial linear model was fitted with the full suite of predictor variables listed in the correlation matrix in Figure 7, with not interaction term, polynomial terms or otherwise transformed variables. While the t-values obtained indicated significant relationships for several of the predictor variables, the DHARMA residual diagnostics revealed significant quantile deviations and the presence of outlier data points. The Multiple R-squared value for this model was 0.2905.

Conversely, the simplified version of the model with highly correlated variables removed yielded a much worse fit and had a lowered Multiple R-squared value of 0.1955, indicating that less of the variability was being explained by the model. The diagnostic tests for this model also showed significant quantile deviations. While significance of the effects of environmental parameters varied between the 2 models, species-specific effects remained significant in both, suggesting that species-specific ecological and physiological differences are important factors influencing growth rates.

The predictor variables were then tested for skewness using the *e1071* package, and log-transformations were applied to mean stream level and mean stream flow variables using the *log1p()* function. Models were also fitted using interaction terms, paying particular attention to the potential differences in how each of the species react to changes in temperature and flow regimes. Alternatively, models were also fitted using species specific subsets to further investigate species specific responses. The results indicated significant positive impacts from mean stream level and

atmospheric temperatures at various life stages for Common Carp and Golden Perch. Conversely, Bony Bream exhibited negative relationships with mean stream level, suggesting potentially differing ecological adaptabilities among species. However, as linear models consistently produced no further improvements in model fit, the modeling method was progressed to GLMs.

2.3.2 General Linear Models

GLMs were fitted on the data with a select set of variables after eliminating variables that contributed to high multi-collinearity. The formula for the base GLM was as follows:

$$E(\text{AnnualGrowthRate}) = \alpha + \beta_1(\log_mean_StreamLvl_m) + \beta_2(\log_mean_StreamFlow_megalitre) + \beta_3(\text{MeanTemp_degC_2yo}) + \beta_4(\text{MeanTemp_degC_1yo}) + \beta_5(\text{MeanTemp_degC_spawning}) + \beta_6(\text{LongestZeroFlow_2yo}) + \beta_7(\text{SpeciesCommonCarp}) + \beta_8(\text{SpeciesGoldenPerch})$$

where:

- α is the intercept representing the average annual growth rate for bony bream,
- β_1 is the coefficient for mean stream level, indicating the change in annual growth rate associated with a one-unit increase in the logarithm of mean stream level.
- β_2 is the coefficient for mean stream flow, indicating the change in annual growth rate associated with a one-unit increase in the logarithm of mean stream flow.
- β_3 to β_5 represent the effects of Mean Temperature at age 2 year, 1 year and spawning, each showing the change in annual growth rate for a one-degree Celsius increase at different life stages.
- β_6 is the coefficient for longest zero flow at age 2 years, reflecting the impact on growth rate per unit increase in the longest duration of zero flow measured at two years old.
- β_7 and β_8 are coefficients for species Common Carp and Golden Perch, respectively, indicating the difference in average growth rates compared to the reference species (intercept) Bony Bream.

While the observations of zero annual growth rate could be ecologically meaningful, GLMs were also fitted with the filtered subset of data that removed all zero annual growth rate counts and NA values. While the latter had no Q-Q plot deviations unlike the former, the quantile deviations in the residuals vs predicted plot persisted in both models. This was also the case for the GLMs with interaction terms and most of the species-specific models, and none of them passed the Pregibon link test except for the Bony Bream GLM with zero counts removed. Alternative versions of the models were also fitted

using the first 3 principal components derived via PCA on the full set of predictor variables except for 'Species'. Having noted no significant improvement in the fit of any of the models, GLMs were then fitted with the same predictors, but with polynomial terms for temperature and longest zero flow. This was repeated for all species, with both versions of the filtered datasets and an immediate improvement in model fit was observed across the board. All GLMs were tested for homoscedasticity, and the Pregibon link test was used to test for misspecification.

2.3.3 Generalized Linear Mixed-Effects Models

I developed Generalized Linear Mixed-Effects Models (GLMMs) using the *lme4* library in R, with random intercepts for species and Site ID. The models were tested with the two versions of the filtered data sets, and species-specific versions of the models were also fitted.

2.3.4 Bayesian General Linear Models

Finally, Bayesian GLMs were fitted for each species using the *brms* package. This approach allowed for the integration of prior knowledge and provided a robust framework for parameter estimation. The Bayesian model also facilitated better handling of uncertainty and was expected to provide richer insights through posterior distributions.

2.3.3 Model Validation

Model validation and comparison was only performed on the top six best models, as per model diagnostics; namely, the 3 species-specific GLMs, and the 3 species-specific Bayesian GLMs. A rigorous k-fold cross-validation approach was implemented, using 10 folds to estimate the generalization error. This involved partitioning the data into ten subsets, and iteratively using nine subsets for training and one for testing. This approach maximized the use of available data while providing a reliable estimate of model performance. Root mean square error (RMSE) and mean absolute error (MAE) was calculated for each fold, using the *caret* library for GLMs and the *brms* package for Bayesian models. The former is more sensitive to larger errors, making it useful for highlighting significant discrepancies, whereas the latter provides a more balanced view of average error magnitude (Hodson 2022). The Bayesian models were specifically formulated to include log

transformations and polynomial terms, reflecting complex variable interactions and non-linear relationships.

3.0 Results

As indicated in Section 2, 6 models were selected from comprehensive suite of models tested, representing the best fits among the various types evaluated. These models were then tested against each other and the results are expressed here:

3.1 Species-Specific GLMs

3.1.1 Golden Perch

The log-transformed mean stream flow in megalitres exhibited a significant positive effect on growth rates (Estimate: 0.008825, t-value: 2.684, p-value: 0.007700), indicating that higher stream flows are associated with increased growth. Additionally, the polynomial term for the mean temperature during the spawning year showed a strong positive effect (Estimate: 1.717803, t-value: 8.103, p-value: 1.56e-14) (see Figure 8). A secondary polynomial term for the same variable also had a significant positive impact (Estimate: 0.411166, t-value: 2.581, p-value: 0.010338). Conversely, the mean temperature in the second year of life displayed a significant negative effect on growth (Estimate: -0.590437, t-value: -2.029, p-value: 0.043373). Additionally, the polynomial term for the mean temperature during the first year was significantly positive (Estimate: 0.969604, t-value: 3.747, p-value: 0.000216), as was the second polynomial term for the longest zero-flow period in the second year with an estimate of 0.701942 (t-value: 4.015, p-value: 7.60e-05).

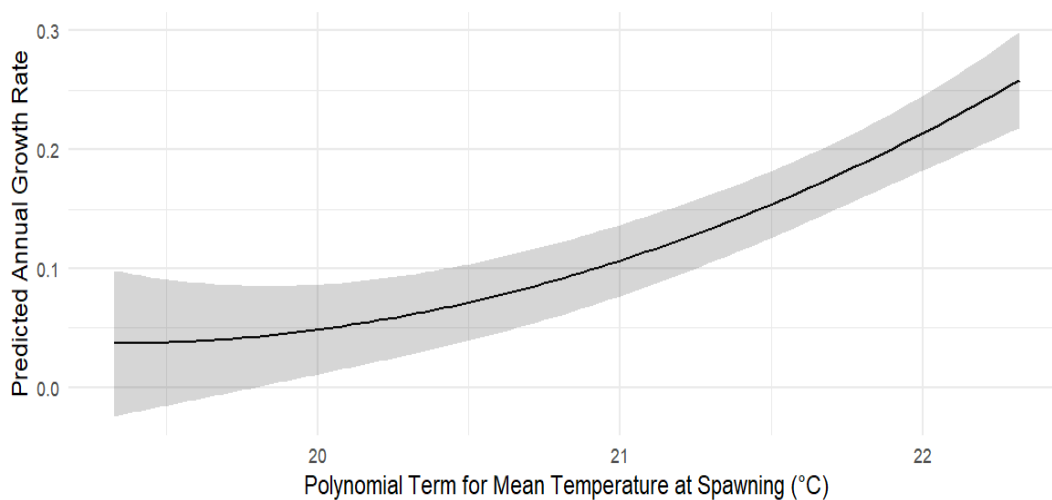
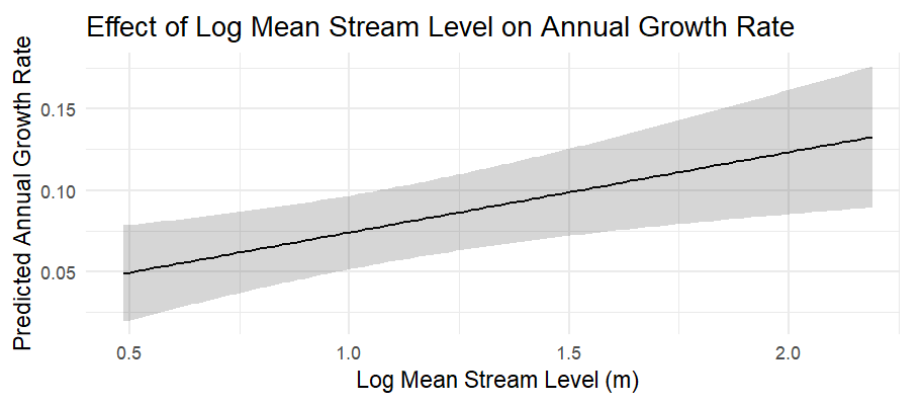


Figure 8: Predicted effect of polynomial term for Mean Temperature at Spawning on Annual Growth rate for Golden Perch

3.1.2 Common Carp

The GLM analysis for Common Carp also highlighted several significant predictors. The log-transformed mean stream level had a significant positive effect on growth (Estimate: 0.049242, t-value: 2.933, p-value: 0.003542). Similarly, log mean streamflow was positively associated with growth (Estimate: 0.007987, t-value: 2.945, p-value: 0.003408). The first polynomial term for the mean temperature during age 2 was significantly positive (Estimate: 0.807874, t-value: 3.430, p-value: 0.000665). Additionally, both polynomial terms for the mean temperature during age 1 were significant, with estimates of 0.817158 (t-value: 4.449, p-value: 1.11e-05) and 0.394370 (t-value: 3.071, p-value: 0.002271), respectively. The polynomial terms for the mean temperature during the spawning year also had significant positive effects on growth, with estimates of 0.985974 (t-value: 5.490, p-value: 7.03e-08) and 0.377328 (t-value: 2.554, p-value: 0.011015). Finally, the second polynomial term for the longest zero-flow period in the second year showed a significant positive effect (Estimate: 0.605876, t-value: 3.876, p-value: 0.000124).

(a)



(b)

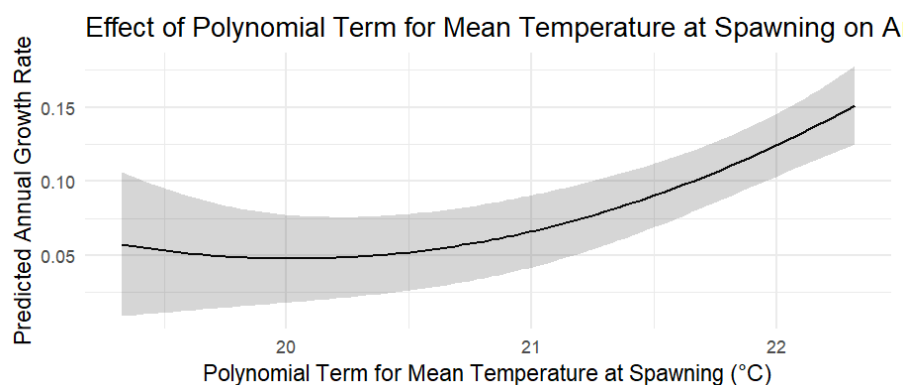


Figure 9: Predicted effect of (a) Log Mean Stream Level and (b) Polynomial Term for Mean Temperature at Spawning on Annual growth rate in Common Carp

3.1.3 Bony Bream

For Bony Bream, the log-transformed mean stream level had a significant negative impact on growth rates (Estimate: -0.24655, t-value: -2.635, p-value: 0.00948), suggesting that higher stream levels are associated with reduced growth. In contrast, log mean streamflow positively affected growth (Estimate: 0.02950, t-value: 2.721, p-value: 0.00743). While the polynomial terms for the mean temperatures in the first and second years, as well as the spawning year, did not show significant effects, the first polynomial term for the longest zero-flow period in the second year had a marginally significant positive effect (Estimate: 1.84284, t-value: 1.884, p-value: 0.06189).

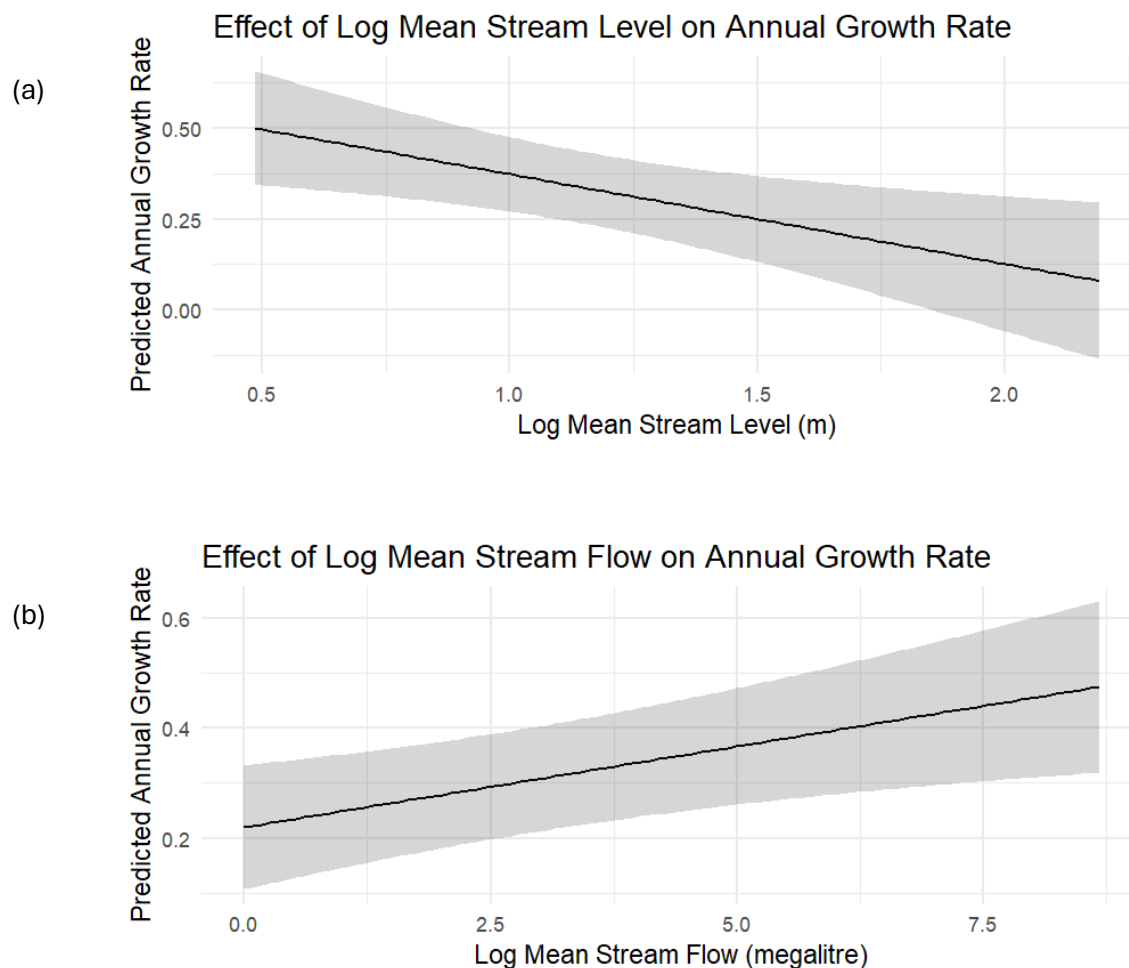


Figure 10: Predicted effect of (a) Log Mean Stream Level and (b) Log Mean Stream Flow on Annual growth rate in Bony Bream

The formulae for these three models can be summarised as below:

$$E(\text{AnnualGrowthRate}) = \alpha + \beta_1(\log_mean_StreamLvl_m) + \beta_2(\log_mean_StreamFlow_megalitre) + \beta_3(\text{MeanTemp_degC_2yo}) + \beta_4(\text{MeanTemp_degC_2yo}^2) + \beta_5(\text{MeanTemp_degC_1yo}) + \beta_6(\text{MeanTemp_degC_1yo}^2) + \beta_7(\text{MeanTemp_degC_spawning}) + \beta_8(\text{MeanTemp_degC_spawning}^2) + \beta_9(\text{LongestZeroFlow_2yo}) + \beta_{10}(\text{LongestZeroFlow_2yo}^2)$$

where:

- α is the intercept representing the average annual growth rate for bony bream,
- β_1 through β_{10} are the coefficients representing the effect sizes of the respective predictor variables,
- $\log_mean_StreamLvl_m$ is the log-transformed mean stream level in meters.
- $\log_mean_StreamFlow_megalitre$ is the log-transformed mean stream flow in megalitres.
- MeanTemp_degC_2yo and $\text{MeanTemp_degC_2yo}^2$ are the first and second polynomial terms for the mean temperature during the second year of life.
- MeanTemp_degC_1yo and $\text{MeanTemp_degC_1yo}^2$ are the first and second polynomial terms for the mean temperature during the first year of life.
- $\text{MeanTemp_degC_spawning}$ and $\text{MeanTemp_degC_spawning}^2$ are the first and second polynomial terms for the mean temperature during the spawning year.
- $\text{LongestZeroFlow_2yo}$ and $\text{LongestZeroFlow_2yo}^2$ are the first and second polynomial terms for the longest zero-flow period during the second year of life.

For the Golden Perch GLM, the Pregibon's Link Test returned a p-value of 0.137, indicating that the model does not suffer from significant misspecification, with an AIC of -632.92 suggesting a good model fit. The Common Carp GLM fitted on the dataset with zero values retained passed the Pregibon's Link Test with a p-value of 0.1456 and achieved an AIC of -903.57, reflecting a strong fit. Similarly, the GLM for Bony Bream also passed the Pregibon's Link Test with a p-value of 0.7821 and had an AIC of -260.73, indicating that the model is well-specified and provides a reasonable fit to the data.

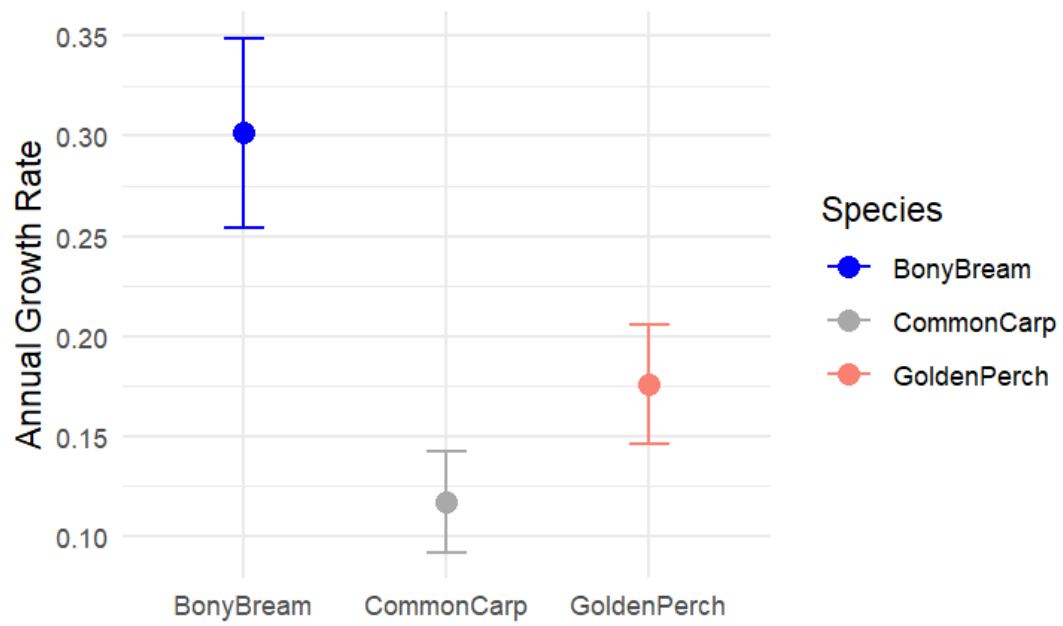


Figure 11: Predicted Annual Growth Rate by Species with 95% Confidence Intervals. The plot shows the fitted values and their corresponding confidence intervals for common carp (CC), golden perch (GP), and bony bream (BB), with points indicating the predicted annual growth rates and error bars representing the confidence intervals.

3.2 Bayesian GLMs

The Bayesian GLMs were fitted with the same terms and base formulae as the regular GLMs. Models ran with four Markov Chain Monte Carlo (MCMC) chains over 2000 iterations each, with a control parameter *adapt_delta* set to 0.95 to increase the sampler's step size adaptivity. The Bayesian GLM for Bony Bream found that log mean stream level had a significant negative effect (Estimate: -0.24, $t = -2.67$), while log mean stream flow showed a positive effect (Estimate: 0.03, $t = 2.92$). The model passed the convergence diagnostics with Rhat values of 1.00 for all parameters, indicating a well-converged model. The residual standard deviation (sigma) was 0.09 with a narrow confidence interval (0.08 to 0.10), suggesting good model fit.

The one for Common Carp showed that log mean stream level (Estimate: 0.03, $t = 2.93$) and log mean stream flow (Estimate: 0.01, $t = 2.95$) had significant positive effects on annual growth. Additionally, temperature during the year before spawning showed significant positive effects, particularly for the first polynomial term (Estimate: 0.81, $t = 8.10$). The model converged well with Rhat values of 1.00 for all parameters. The residual standard deviation (sigma) was 0.07.

The Bayesian GLM for Golden Perch revealed that log mean stream flow had a significant positive effect (Estimate: 0.01, $t = 2.68$), and temperature during spawning had strong positive effects for both polynomial terms (first term Estimate: 0.97, $t = 8.10$; second term Estimate: 0.41, $t = 2.58$). The model showed good convergence with Rhat values of 1.00. The residual standard deviation (sigma) was 0.08.

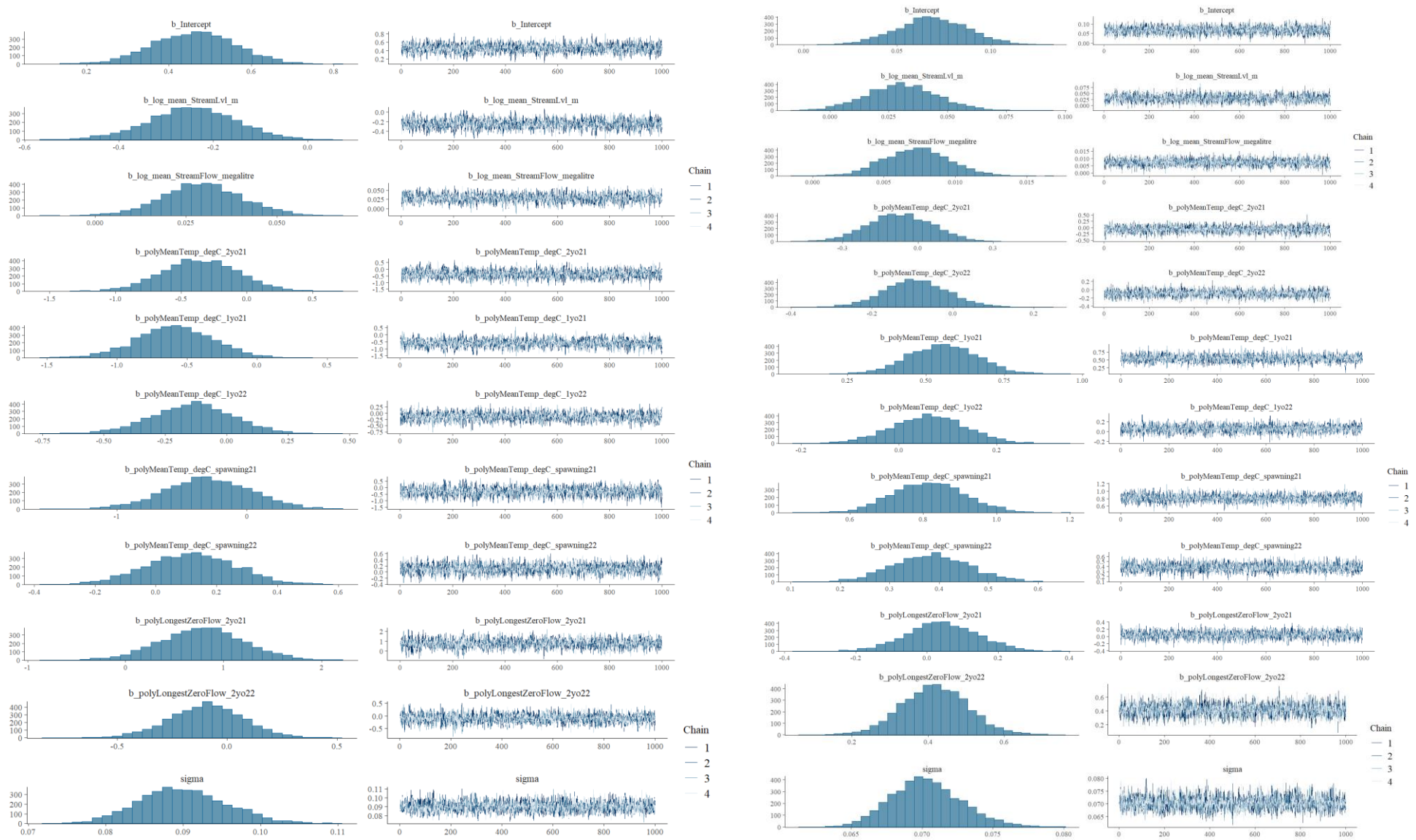


Figure 12: Trace plots and posterior distributions of the Bayesian GLM model for Bony Bream (left) and Common Carp (right). The trace plots indicate good mixing of the MCMC chains and convergence ($Rhat = 1$). The posterior distributions provide the credible intervals for each parameter estimate.

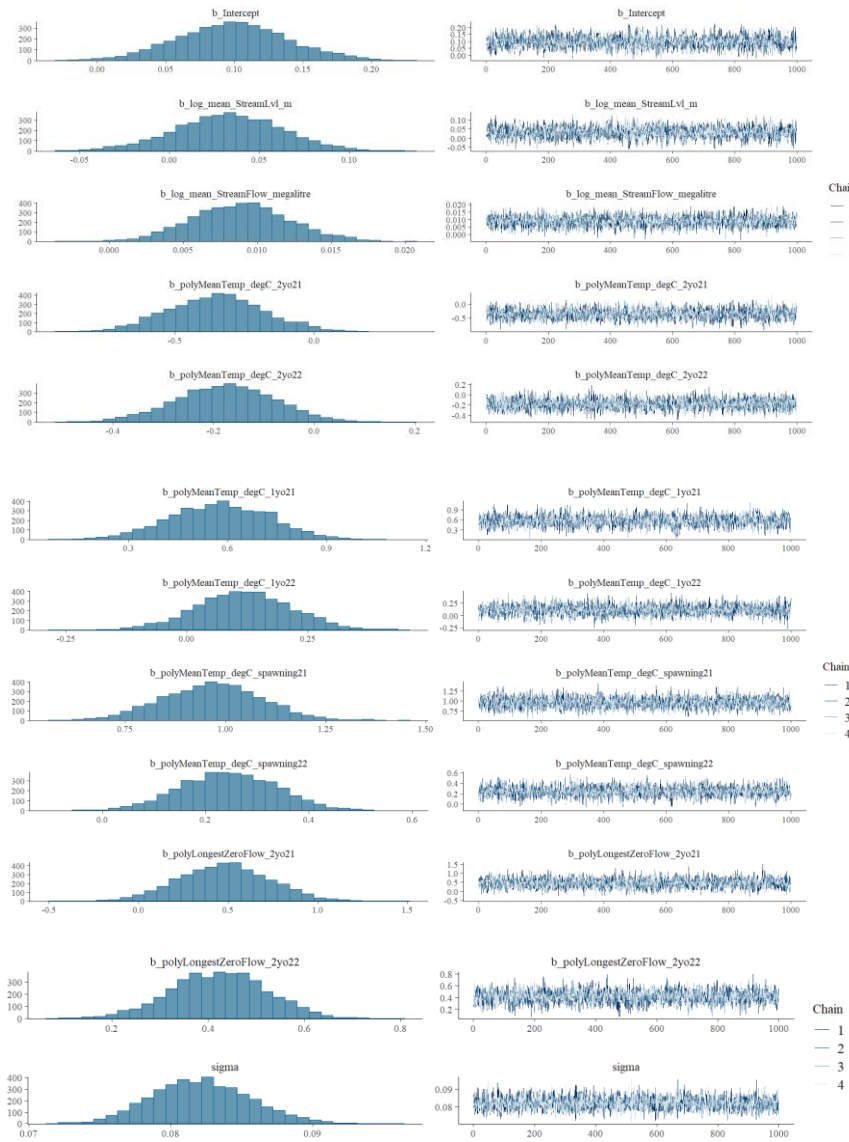


Figure 11 (cont.): Trace plots and posterior distributions of the Bayesian GLM model for Golden Perch. The trace plots indicate good mixing of the MCMC chains and convergence ($R_{hat} = 1$).

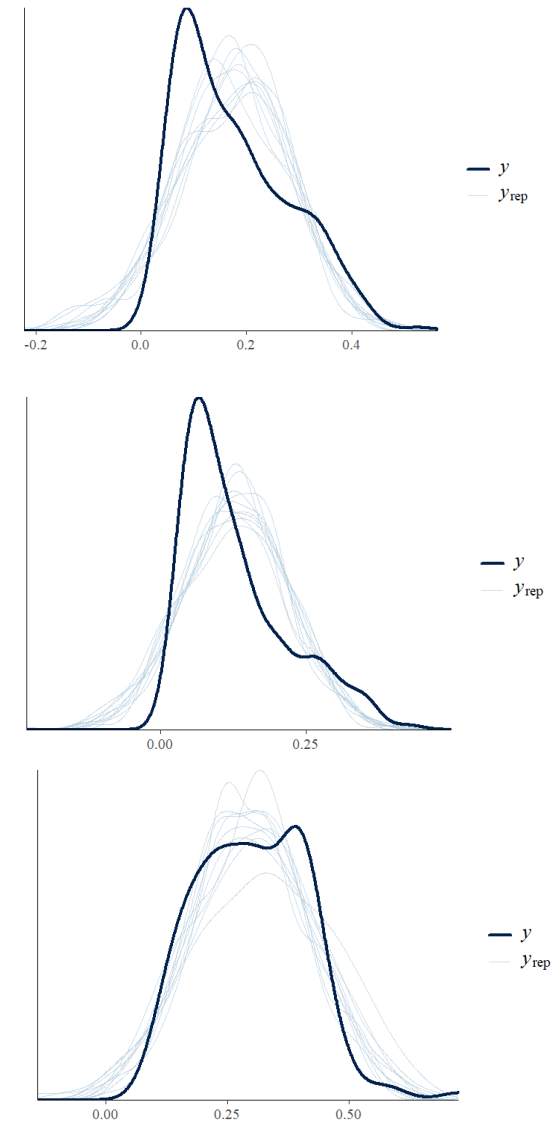


Figure 13: Posterior predictive check (PPC) comparing the observed data (y) and the predicted data (y_{rep}) from the Bayesian GLM models. The PPC plot demonstrates that the model's predictions align well with the observed data, indicating good model fit. From top to bottom: Golden Perch, Common Carp, Bony Bream

3.4 Model Comparison

The performance of the models was evaluated using Root Mean Squared Error (RMSE) and Mean Absolute Error (MAE). The Bony Bream GLM model outperformed the Bayesian model with a lower RMSE (0.0931 vs. 0.1961) and MAE (0.0730 vs. 0.1649). Similarly, the Common Carp GLM model showed better performance with an RMSE of 0.0701 compared to 0.1280 for the Bayesian model and an MAE of 0.0542 compared to 0.1028. And the Golden Perch GLM model also demonstrated superior performance with an RMSE of 0.0824 and an MAE of 0.0633, whereas the Bayesian model had higher error metrics (RMSE: 0.1535, MAE: 0.1248).

MODEL	MODEL TYPE	RMSE	MAE
BONY BREAM	GLM	0.0931	0.0730
BONY BREAM	Bayesian	0.1961	0.1649
COMMON CARP	GLM	0.0701	0.0542
COMMON CARP	Bayesian	0.1280	0.1028
GOLDEN PERCH	GLM	0.0824	0.0633
GOLDEN PERCH	Bayesian	0.1535	0.1248

Table 2: Results of evaluating the model performance of the top 6 models via Root Mean Squared Error (RMSE) and Mean Absolute Error (MAE)

4.0 Discussion

As stated previously, the aim of this report and the associated analysis was to investigate the effect of different environmental and hydrological variables on annual growth rate in Golden perch, Bony bream and Common carp. The results demonstrated clear interspecific differences in growth rates across the majority of the models, with Common carp and Golden perch exhibited significantly lower growth rates compared to Bony bream. Notably, the Bony bream, *N. erebi*, is the most widely distributed freshwater fish in Australia, thus indicating that the species may have high tolerances and is highly adapted to a wide range of conditions, in terms of environmental parameters (Pratt et al. 2024). The bony bream is also known to be relatively abundant following floodplain inundation, as the species has an active dispersal strategy during flooding and is known to reproduce on floodplains (Balcombe et al. 2006) and exhibit higher growth rates in periods of higher temperature, such as summer (Stocks et al. 2019), therefore this the bony bream may simply be in a more advantageous position given the nature of the habitat that is being studied. Furthermore, the common carp is known to grow faster in lentic habitats as opposed to lotic ones, and grows more in cold and temperate climates rather than arid to semi-arid climates, as was the case here (Vilizzi and Copp 2017). Furthermore, previously, studies have also identified movement patterns for golden perch, that includes migrations between the Darling River and the Lower Murray (Zampatti et al. 2021). The increasingly extreme and frequent drought conditions, such as the event preceding the study period, likely restricted their movements, constraining access to optimal habitats necessary for growth and reproduction. Such restrictions highlight the vulnerability of migratory species to extreme climatic events, which are predicted to increase in frequency and intensity.

The findings of this study highlight the interspecific differences in the drivers of fish growth in dryland river systems. Understanding the various aspects of species' life history strategies, habitat preferences, and physiological tolerances that drive these changes could be critical to informing future management endeavours. Furthermore, the insights gained through following this line of questioning can also be used to manage populations of

invasive species such as Common carp, especially given that stream flow variables significantly impact growth rates in this species.

Additionally, the study highlights the importance of considering the cumulative and interactive effects of multiple environmental factors in managing these ecosystems. Single-factor management approaches may be insufficient to address the complexities of dryland river habitats. Instead, integrated management strategies that account for hydrological variability, habitat connectivity, and species interactions are likely to be more effective in ensuring the sustainability of these ecologically and economically important systems.

This research opens several avenues for future investigations, especially with regards to biotic factors such as food availability, predation pressure, and competition, could provide a more comprehensive understanding of the drivers of growth. Studies that integrate ecological interactions with abiotic factors are likely to yield deeper insights into the mechanisms governing fish growth in dryland rivers.

Lastly, exploring the genetic and physiological adaptations of different species to environmental stressors could offer valuable information on their resilience and adaptive capacities. Such research could inform conservation strategies aimed at enhancing the resilience of fish populations to future climate variability and change.

Supplementary Material

Note: All code used during this analysis is available via: <https://github.com/HawwaNizar/QBIO7008-ANALYSING-THE-EFFECT-OF-ENVIRONMENTAL-VARIABILITY-ON-FISH-GROWTH-RATES-IN-QLD>

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